

Fig. 1

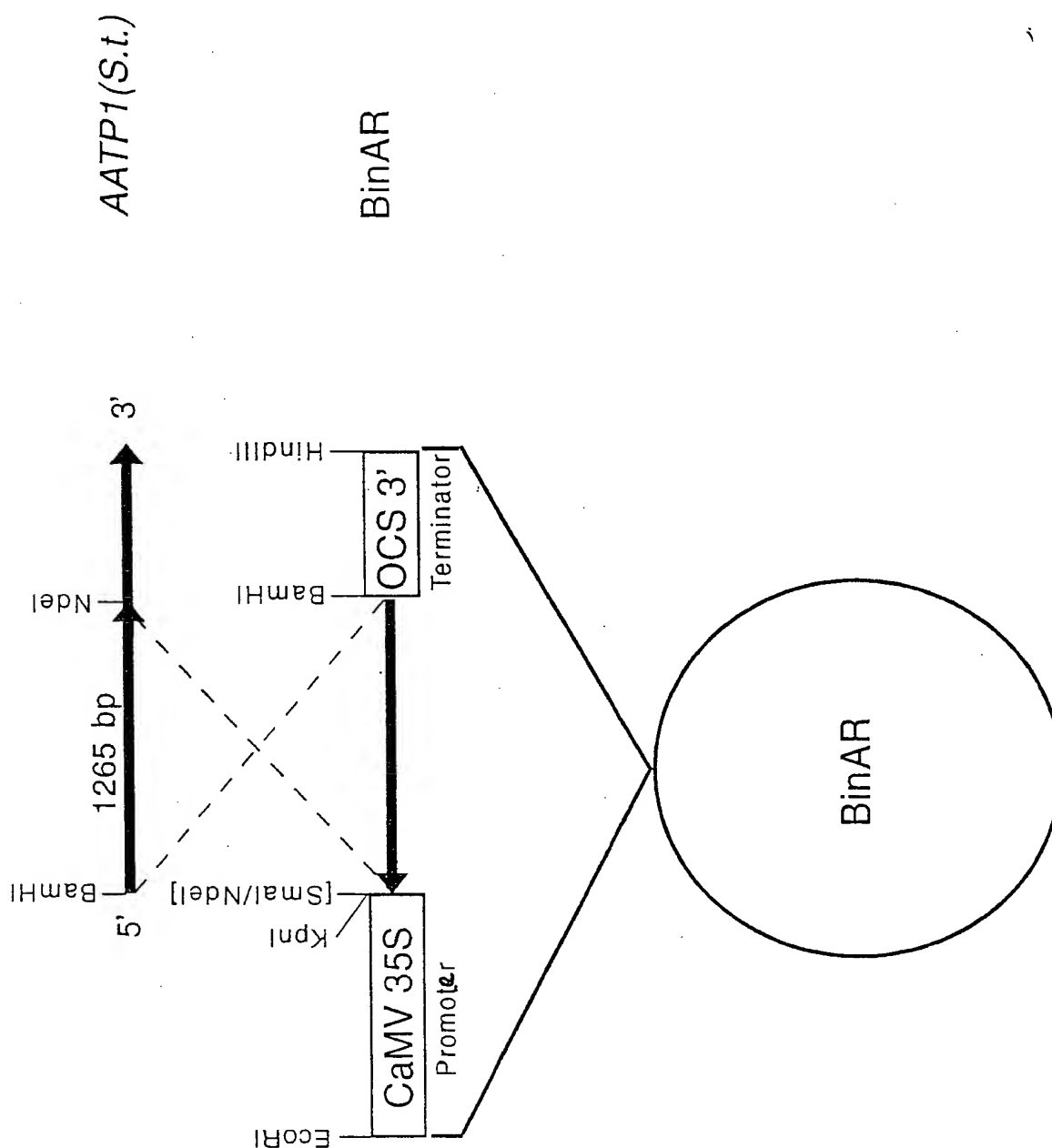


Fig. 2

DC Alignment:

3/8

- 1 AATP1_A.T._
- 2 AATP2_A.t._
- 3 TLC_

10 20 30 40 50 60
 1 MEAVIQTRGLLSLPTKPIGVRSQQLPSHGLKQRLFAAKPRNLHGCLYPLTGTRNFKPLSQ 60
 2 MEGLIQTRGILSLPASHR-SEKVLQPSHGLKQRLFTTN---LPALSLSLMVTRNFKPFSK 56
 3 -----MS-----TSK-----SENY--LS- 11

70 80 90 100 110 120
 1 PCMGFRFPTKREAPSSYARRRRGCWRRSCLRRSDSAAVVASRKIFGVEVATLKKIPLGL 120
 2 SHLGFRFPTRREAEDSLARRKLRRPRKCVDEGDTAAMAVSPKIFGVEVTTLKKIVPLGL 116
 3 -----EL-----RKIWP-----IEQYENKKFLPLAF 33

130 140 150 160 170 180
 1 MFFCILFNITLRTDKDVLVVTAKGSSAEIIPFLKTWVNLPMAGFMLLYTKLSNVLSKK 180
 2 MFFCILFNITLRTDKDVLVVTAKGSSAEIIPFLKTWVNLPMAGFMLLYTKLSNVLSKK 176
 3 MMFCILLNYSTLRSIKDGFVVDIG-T-ESISFLKTYIVLPSAVIAMIIYVKLCDILKQE 91

190 200 210 220 230 240
 1 ALFYTVIVPFIHYFGFGFVVMYPLSNYIHPEALADKLLTTLGPRFMGPAILRIWSFCLF 240
 2 ALFYTVIVPFIYVYFGAFGVMYPRSNLIQPEALADKLLATLGPFRMGPLAIMRIWSFCLF 236
 3 NVFYVITSFFLGYFALFAFVLYPYPDLVHPDHKTIESLSLAYPNFKWFIKIVGKWSFASF 151

250 260 270 280 290 300
 1 YVMAELWGSVVSVLFWGFANQITTVDEAKKFYPLFGIGANVALIFSGRTVKYFSNLRKN 300
 2 YVMAELWGSVVSVLFWGFANQITTVDEAKKFYPLFGLGANVALIFSGRTVKYFSNMRKN 296
 3 YTIAELWGTMMLSLLFWQFANQITKIAEAKRFYSMFGLLANLALPVTSSVIGYFLHEKTQ 211

310 320 330 340 350 360
 1 LGPGVDGSFV--ESHDEHCGNGTRICLSIGGSNRYV---P-L--PTRSKNKKEKPKMGT 352
 2 LGPGVDGWAVSLKAMMSIVVGMGLAICFLYWWVNRVYV---P-L--PTRSKKKKVKPQMGT 350
 3 I-VAEHLKFV---PLFVIMITSSFLIILTIRWMNKNVLTDPRLYDPALVKEKKTAKLSF 267

370 380 390 400 410 420
 1 MESLKFLVSSPYIRDLATLVVAYGISINLVEVTWKSCLKAQFSPNEYSAFMGAFSTCTG 412
 2 MESLKFLVSSPYIRDLATLVVAYGISINLVEVTWKSCLKSQFSPNEYSAFMGDFSTCTG 410
 3 IESLKMIFTSKYVGYIALIIAYGVSVINLVEGVWKS VKELYPTKEAYTIYMGQFQFYQG 327

430 440 450 460 470 480
 1 VATFTMMLLSQYVFNKYGWGVAAKITPTVLLLTGVAFFSLILFGGPFA-PLVAKLGMTPL 471
 2 IATFTMMLLSQYVFKKYGWGVAAKITPTVLLLTGVAFFSLILFGGPFA-PLVAKLGMTPL 469
 3 WVAIAFMLIGSNILRKVSWLTAAMITPLMMFITGAFFSFIFFDSVIAMNLTGILASSPL 387

490 500 510 520 530 540
 1 LAAVYVGALQNIFSK-SAKYSLFDPCKEMAYIPLDEDTKVKGKAAIDVVCNPLGKSGGAL 530
 2 LAAVYVVPPEVSSARVQVQHSSTPSAMQECLYPLDEVSKVKAKLQL-MWSATIGKSGGAL 528
 3 TLAVMIGMIQNVLSK-GVKYSLFDTKNMAYIPLDKDLRVKGQA AAVEVIGGRLGKSGGAI 446

550 560 570 580 590 600
 1 IQQ-FMIL--SFGSLANSTPYLGMILLVIVTAWLAAAKSLEGQFNSLRLKSLRRKWREL 587
 2 IQQ-FMIL--TFGSLANSTPYLGIVTAWLAAAKSLEGPV----- 569
 3 IQSTFFILFPVFGFI-EATPYFASIFFIIVILWIFAVKGLNKEYQVL-VNKNEK----- 498

1 HR 589
 2 -- 569
 3 -- 498

Fig. 3

4/8

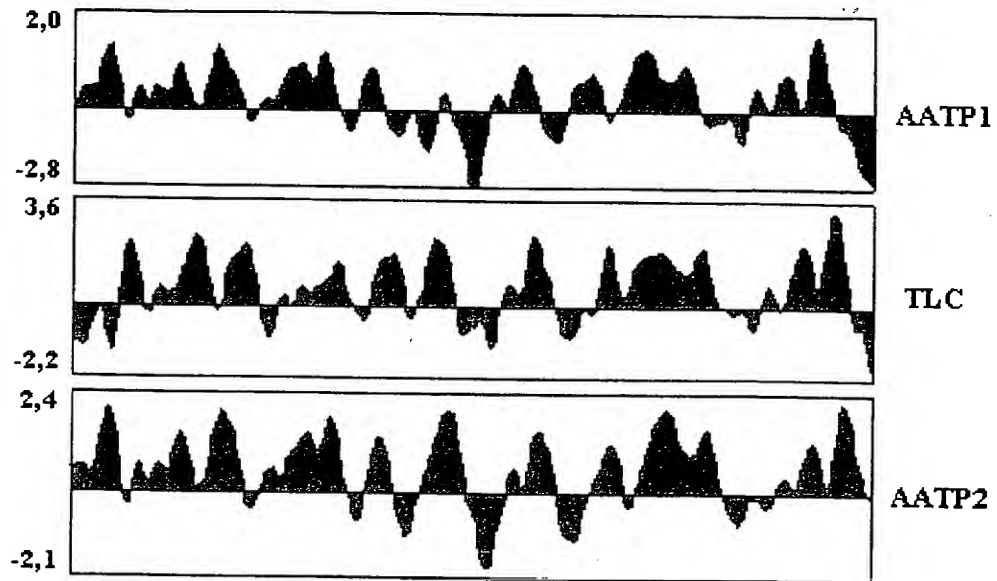


Fig. 4

5/8

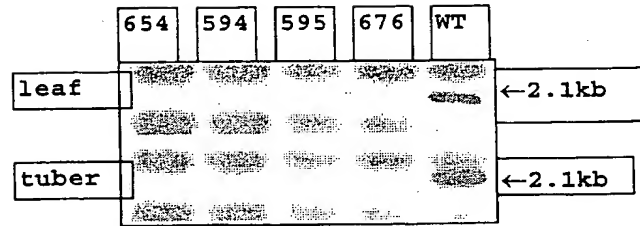


Fig. 5

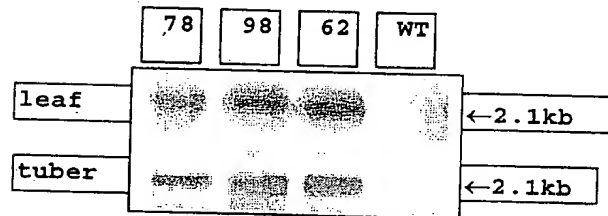


Fig. 6

6/8

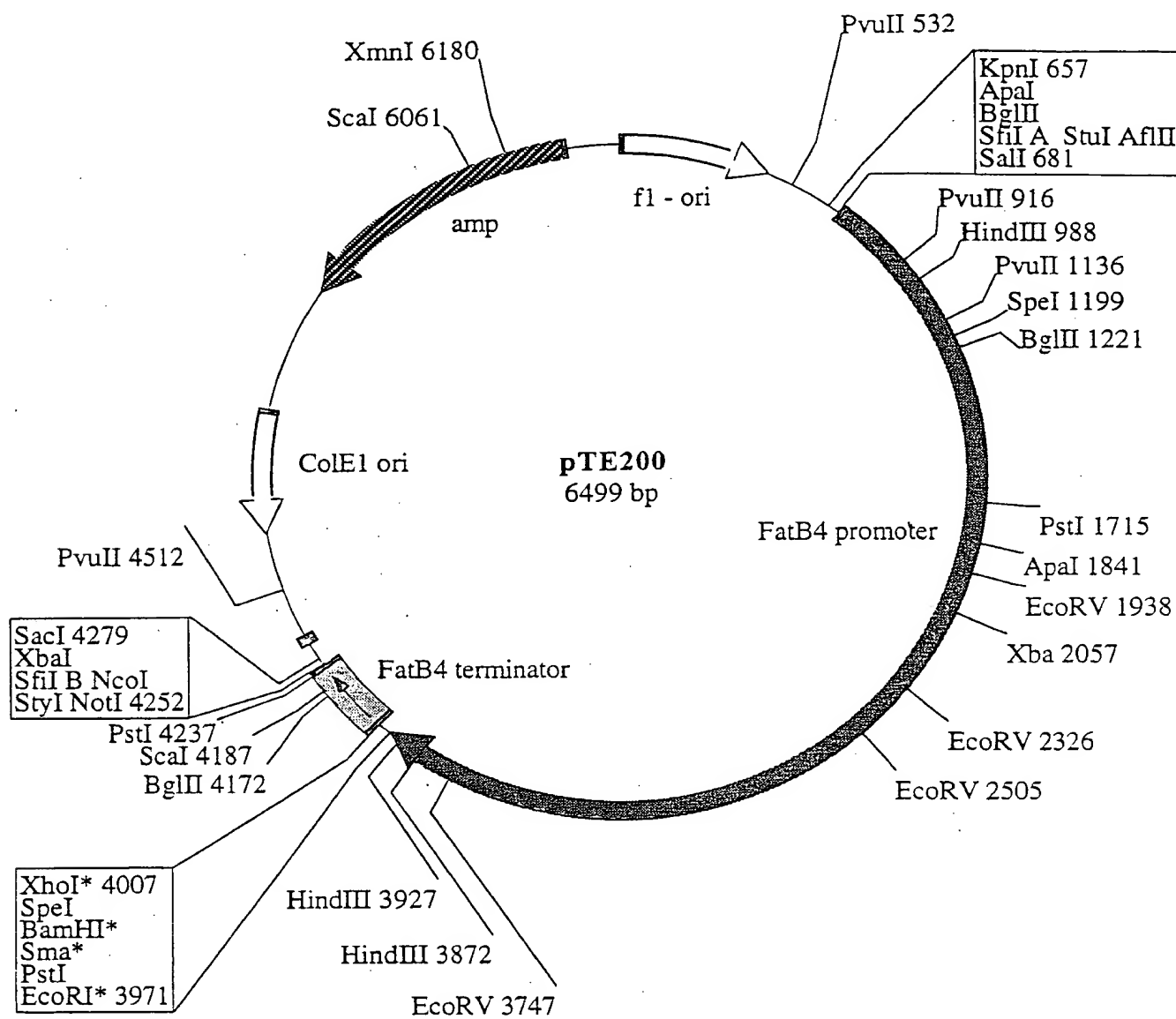


Fig. 7

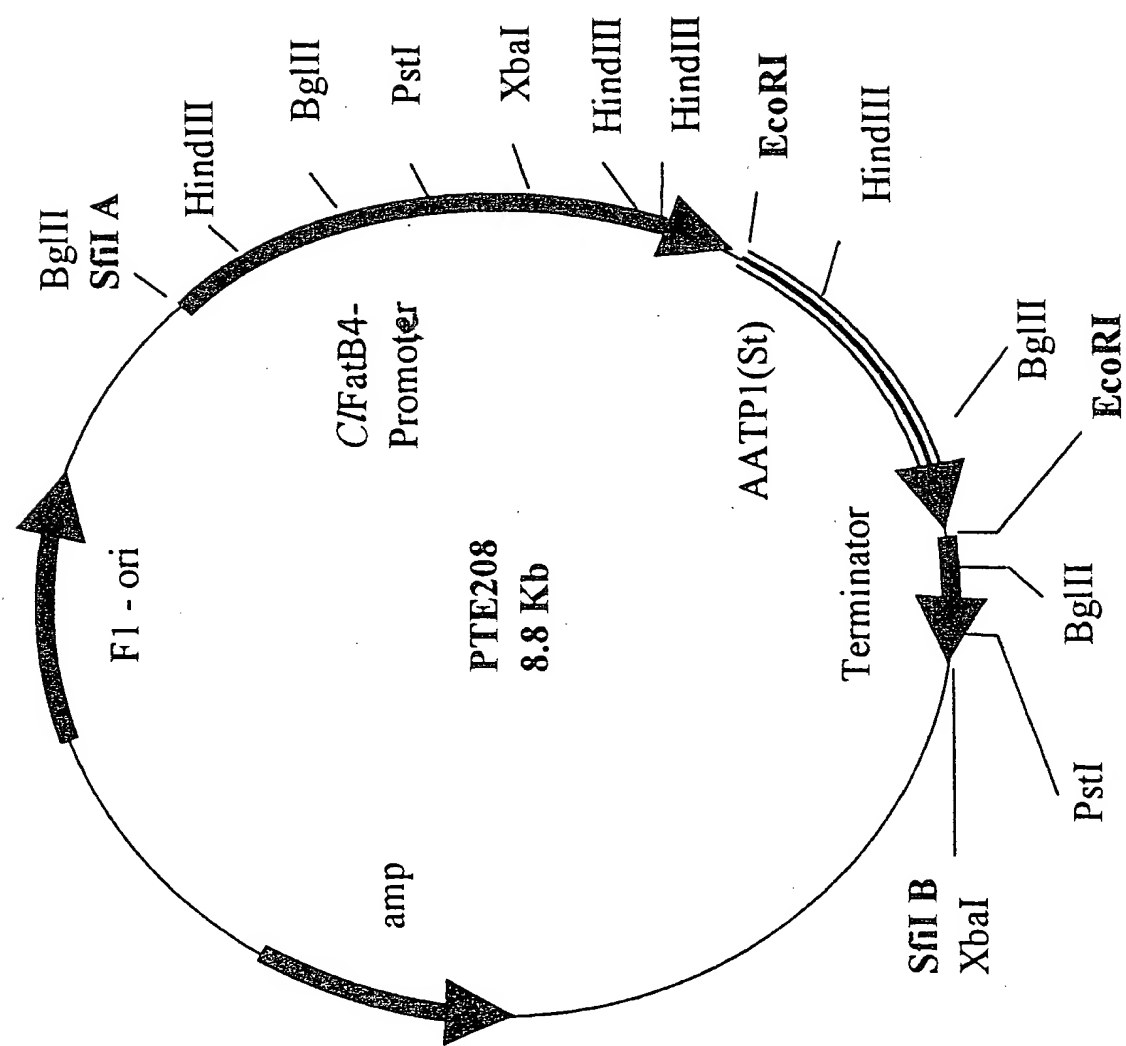


Fig. 8

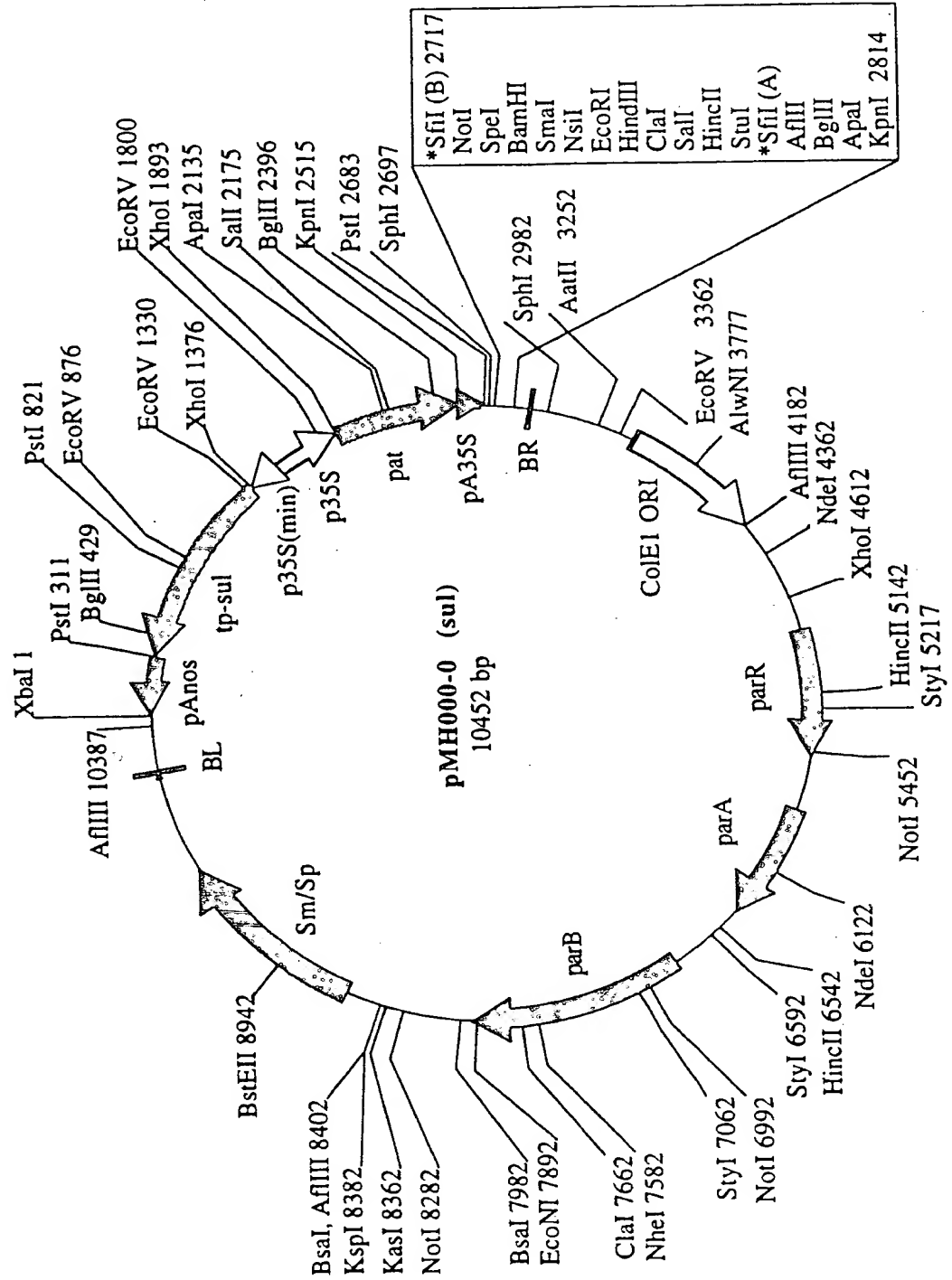


Fig. 9